SCORE Search Results Details for Application 10680755 and Search Result us-10-680-755a-1.olig.rst.

This page gives you Search Results detail for the Application 10680755 and Search Result us-10-680-755a-1.olig.rst.

```
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OM nucleic - nucleic search, using sw model

Run on:          June 19, 2006, 21:15:04 ; Search time 7702 Seconds
                                           (without alignments)
                                           10861.506 Million cell updates/sec

Title:           US-10-680-755A-1
Perfect score:   1496
Sequence:        1 cgcccttactcactataggg..........aaaaaaaatatgcggccgcg 1496

Scoring table:   OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched:        48236798 seqs, 27959665780 residues

Word size :      1

Total number of hits satisfying chosen parameters:      96473154

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :       EST:*
                 1:   gb_est1:*
                 2:   gb_est3:*
                 3:   gb_est4:*
                 4:   gb_est5:*
                 5:   gb_est6:*
                 6:   gb_htc:*
                 7:   gb_est2:*
                 8:   gb_est7:*
                 9:   gb_est8:*
                 10:  gb_est9:*
                 11:  gb_gss1:*
                 12:  gb_gss2:*
                 13:  gb_gss3:*
                 14:  gb_gss4:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	451	30.1	569	9	DB312688	DB312688 DB312688
	2	436	29.1	624	9	DR006966	DR006966 TC118886
	3	410	27.4	468	4	BX115959	BX115959 BX115959
c	4	404	27.0	404	1	AI277349	AI277349 qm54a05.x
c	5	371	24.8	457	1	AI718823	AI718823 at15h12.x
	6	231	15.4	231	14	AY406752	AY406752 Homo sapi
	7	231	15.4	231	14	AY406753	AY406753 Pan trogl
c	8	221	14.8	419	7	AW082911	AW082911 xc04c10.x
c	9	147	9.8	323	7	BE242960	BE242960 TCAAP2D23
	10	45	3.0	782	5	CJ483386	CJ483386 CJ483386
c	11	39	2.6	251	10	DW287236	DW287236 LRAGE0420
	12	39	2.6	301	10	DW336914	DW336914 LRAGE0498
c	13	39	2.6	308	10	DW290825	DW290825 LRAGE0536
	14	39	2.6	462	8	CR790659	CR790659 DKFZp459H
	15	39	2.6	704	10	DW398992	DW398992 LRAGE0413
	16	38	2.5	197	10	DW286754	DW286754 LRAGE0416
	17	38	2.5	233	10	DT948983	DT948983 15-1-63 S
c	18	38	2.5	280	10	DW308948	DW308948 LRAGE0437
c	19	38	2.5	288	10	DW320319	DW320319 LRAGE0451
c	20	38	2.5	296	10	DW334349	DW334349 LRAGE0473
c	21	38	2.5	301	10	DW337533	DW337533 LRAGE0504
c	22	38	2.5	303	10	DW287823	DW287823 LRAGE0506
c	23	38	2.5	308	10	DW292233	DW292233 LRAGE0550
	24	38	2.5	310	10	DW376866	DW376866 LRAGE0217
c	25	38	2.5	311	1	AJ316137	AJ316137 AJ316137
c	26	38	2.5	311	10	DW292018	DW292018 LRAGE0548
	27	38	2.5	327	10	DW378920	DW378920 LRAGE0233
c	28	38	2.5	340	10	DW380124	DW380124 LRAGE0246
	29	38	2.5	342	10	DW308678	DW308678 LRAGE0705
	30	38	2.5	342	10	DW308679	DW308679 LRAGE0705
	31	38	2.5	356	10	DW315560	DW315560 LRAGE0763
c	32	38	2.5	379	10	DW383213	DW383213 LRAGE0281
	33	38	2.5	424	10	DW393597	DW393597 LRAGE0314
c	34	38	2.5	451	10	DW389549	DW389549 LRAGE0334
	35	38	2.5	454	10	DW389725	DW389725 LRAGE0336
	36	38	2.5	466	10	DW331764	DW331764 LRAGE0905
	37	38	2.5	502	10	DW332691	DW332691 LRAGE0915
	38	38	2.5	539	10	DW392784	DW392784 LRAGE0382
	39	38	2.5	554	10	DW393209	DW393209 LRAGE0387
	40	38	2.5	623	10	DW398148	DW398148 LRAGE0405
c	41	37	2.5	116	4	CA923240	CA923240 EST00012
c	42	37	2.5	169	10	DW364211	DW364211 LRAGE0096
c	43	37	2.5	191	8	CV888764	CV888764 LRRGE0065
	44	37	2.5	252	8	CV699404	CV699404 Litsty 02
c	45	37	2.5	269	10	DW297989	DW297989 LRAGE0428
	46	37	2.5	269	10	DW372496	DW372496 LRAGE0179
c	47	37	2.5	271	8	CX274383	CX274383 EX20LIB4_
c	48	37	2.5	283	10	DW309218	DW309218 LRAGE0440
c	49	37	2.5	286	10	DW319816	DW319816 LRAGE0446
	50	37	2.5	287	10	DW320085	DW320085 LRAGE0449
c	51	37	2.5	288	10	DW320332	DW320332 LRAGE0451

SCORE Search Results Details for Application 10680755 and Search Result us-10-680-755a-1.olig-n2p.rag.

This page gives you Search Results detail for the Application 10680755 and Search Result us-10-680-755a-1.olig-n2p.rag.

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OM nucleic - protein search, using frame_plus_n2p model

Run on:          June 20, 2006, 07:56:31 ; Search time 52.1 Seconds
                                           (without alignments)
                                           3938.555 Million cell updates/sec

Title:           US-10-680-755A-1
Perfect score:   480
Sequence:        1 cgcccttactcactataggg..........aaaaaaaatatgcggccgcg 1496

Scoring table:   OLIGO
                 Xgapop 60.0 , Xgapext 60.0
                 Ygapop 60.0 , Ygapext 60.0
                 Fgapop 60.0 , Fgapext  7.0
                 Delop  60.0 , Delext  60.0

Searched:        2589679 seqs, 457216429 residues

Word size:       1

Total number of hits satisfying chosen parameters:       4838484

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10680755/runat_19062006_173213_21451/app_query.fasta_1
-DB=A_Geneseq -QFMT=fastan -SUFFIX=olig-n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=100 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=50 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10680755_@CGN_1_1_364_@runat_19062006_173213_21451 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60
```

```
Database :        A_Geneseq_8:*
                  1:  geneseqp1980s:*
                  2:  geneseqp1990s:*
                  3:  geneseqp2000s:*
                  4:  geneseqp2001s:*
                  5:  geneseqp2002s:*
                  6:  geneseqp2003as:*
                  7:  geneseqp2003bs:*
                  8:  geneseqp2004s:*
                  9:  geneseqp2005s:*
                  10:  geneseqp2006s:*


       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.
```

                            SUMMARIES

		% Query				
Result No.	Score	Match	Length	DB	ID	Description
1	108	22.5	108	4	AAB68426	Aab68426 Amino aci
2	108	22.5	108	5	ABG94397	Abg94397 Human GPC
3	108	22.5	108	5	AAO15531	Aao15531 Human phy
4	108	22.5	108	5	AAE24384	Aae24384 Human pro
5	108	22.5	108	6	ABU07602	Abu07602 Human ZVE
6	108	22.5	108	6	AAE36789	Aae36789 Human Bv8
7	108	22.5	108	7	ADD69039	Add69039 Human Bv8
8	108	22.5	108	7	ADF28067	Adf28067 Human Zve
9	108	22.5	108	7	ABG75087	Abg75087 Human pro
10	108	22.5	108	7	ADJ71811	Adj71811 Human pro
11	108	22.5	108	8	ADN41839	Adn41839 Amino aci
12	108	22.5	108	8	ADO24421	Ado24421 Human PRO
13	108	22.5	108	8	ADS86957	Ads86957 Human Zve
14	108	22.5	108	8	ADS00460	Ads00460 Human Bv8
15	108	22.5	108	8	ADS86495	Ads86495 Human BV8
16	108	22.5	108	8	ADS75496	Ads75496 Human pro
17	108	22.5	108	9	AEA23706	Aea23706 Human PRO
18	108	22.5	108	9	AEB45585	Aeb45585 Human Zve
19	108	22.5	108	9	AED08085	Aed08085 Human Zve
20	108	22.5	116	8	ADN41861	Adn41861 Amino aci
21	108	22.5	116	8	ADS86981	Ads86981 Human Zve
22	87	18.1	100	9	ADY86166	Ady86166 Human Bv8
23	81	16.9	81	5	ABG94398	Abg94398 Human GPC
24	81	16.9	81	5	AAO15530	Aao15530 Human phy
25	81	16.9	81	5	AAE24385	Aae24385 Human pro
26	81	16.9	81	7	ADD69041	Add69041 Human Bv8
27	81	16.9	81	7	ADO05356	Ado05356 Human maj
28	81	16.9	81	8	ADN43258	Adn43258 Amino aci
29	81	16.9	81	8	ADR24005	Adr24005 Human ZAQ
30	81	16.9	81	8	ADS86493	Ads86493 Human BV8
31	81	16.9	81	8	ADS75497	Ads75497 Human pro
32	81	16.9	81	9	ADW00755	Adw00755 Amino aci
33	81	16.9	81	9	ADZ88900	Adz88900 Human pro
34	81	16.9	81	9	ADZ58574	Adz58574 Human ZAQ
35	81	16.9	81	9	AEB45593	Aeb45593 Human Zve
36	81	16.9	81	9	AED00597	Aed00597 Human pro
37	80	16.7	80	5	ABG94400	Abg94400 C-termina
38	80	16.7	80	7	ADD69044	Add69044 Human Bv8
39	74	15.4	129	6	AAE36788	Aae36788 Human Bv8
40	74	15.4	129	7	ADJ71815	Adj71815 Human pro

This page gives you Search Results detail for the Application 10680755 and Search 680-755a-1.olig-n2p.rai.

start

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OM nucleic - protein search, using frame_plus_n2p model

Run on:         June 20, 2006, 08:21:41 ; Search time 11.5 Seconds
                                          (without alignments)
                                          3415.978 Million cell updates/sec

Title:          US-10-680-755A-1
Perfect score:  480
Sequence:       1 cgcccttactcactataggg..........aaaaaaaatatgcggccgcg 1496

Scoring table:  OLIGO
                Xgapop 60.0 , Xgapext 60.0
                Ygapop 60.0 , Ygapext 60.0
                Fgapop 60.0 , Fgapext  7.0
                Delop  60.0 , Delext  60.0

Searched:       650591 seqs, 87530628 residues

Word size:      1

Total number of hits satisfying chosen parameters:      1153298

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10680755/runat_19062006_173219_21533/app_query.fasta_1
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=olig-n2p.rai -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=50 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02p
-USER=US10680755_@CGN_1_1_78_@runat_19062006_173219_21533 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60
```

```
Database :        Issued_Patents_AA:*
                  1:  /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
                  2:  /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
                  3:  /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
                  4:  /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
                  5:  /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
                  6:  /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
                  7:  /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                        SUMMARIES

                          %
    Result              Query
      No.    Score    Match  Length  DB   ID                        Description
    -----------------------------------------------------------------------------
         1    108      22.5    108    2   US-09-712-529-2           Sequence 2, Appli
         2    108      22.5    108    2   US-10-212-201A-2          Sequence 2, Appli
         3    108      22.5    108    2   US-10-212-355-2           Sequence 2, Appli
         4     12       2.5    689    2   US-09-106-194-2           Sequence 2, Appli
         5     12       2.5    999    2   US-09-747-371-2           Sequence 2, Appli
         6     11       2.3    504    2   US-09-949-016-7020        Sequence 7020, Ap
         7     11       2.3    504    2   US-09-991-181-119         Sequence 119, App
         8     11       2.3    504    2   US-09-990-444-119         Sequence 119, App
         9     11       2.3    504    2   US-09-997-333-119         Sequence 119, App
        10     11       2.3    504    2   US-09-992-598-119         Sequence 119, App
        11     11       2.3    504    2   US-09-989-735-119         Sequence 119, App
        12     11       2.3    504    3   US-09-989-726-119         Sequence 119, App
        13     11       2.3    504    3   US-09-997-514-119         Sequence 119, App
        14     11       2.3    504    3   US-09-989-728-119         Sequence 119, App
        15     11       2.3    504    3   US-09-997-349-119         Sequence 119, App
        16     11       2.3    504    3   US-09-997-653-119         Sequence 119, App
        17     11       2.3    504    3   US-09-989-293A-119        Sequence 119, App
        18     11       2.3    511    2   US-09-949-016-10054       Sequence 10054, A
  c     19     11       2.3    776    2   US-10-020-079-24          Sequence 24, Appl
  c     20     11       2.3    776    2   US-10-413-437-24          Sequence 24, Appl
  c     21     11       2.3    789    2   US-10-020-079-22          Sequence 22, Appl
  c     22     11       2.3    789    2   US-10-413-437-22          Sequence 22, Appl
  c     23     11       2.3    863    2   US-10-020-079-32          Sequence 32, Appl
  c     24     11       2.3    863    2   US-10-413-437-32          Sequence 32, Appl
  c     25     11       2.3    876    2   US-10-020-079-30          Sequence 30, Appl
  c     26     11       2.3    876    2   US-10-413-437-30          Sequence 30, Appl
  c     27     11       2.3    889    2   US-10-020-079-20          Sequence 20, Appl
  c     28     11       2.3    889    2   US-10-413-437-20          Sequence 20, Appl
  c     29     11       2.3    895    2   US-10-020-079-18          Sequence 18, Appl
  c     30     11       2.3    895    2   US-10-413-437-18          Sequence 18, Appl
  c     31     11       2.3    976    2   US-10-020-079-28          Sequence 28, Appl
  c     32     11       2.3    976    2   US-10-413-437-28          Sequence 28, Appl
  c     33     11       2.3    982    2   US-10-020-079-26          Sequence 26, Appl
  c     34     11       2.3    982    2   US-10-413-437-26          Sequence 26, Appl
        35     11       2.3    997    2   US-09-747-371-3           Sequence 3, Appli
        36     10       2.1    146    2   US-09-893-737-42          Sequence 42, Appl
        37     10       2.1    476    2   US-09-949-016-11726       Sequence 11726, A
        38     10       2.1    684    1   US-08-555-669-12          Sequence 12, Appl
        39     10       2.1    684    2   US-09-073-663-12          Sequence 12, Appl
  c     40     10       2.1    689    2   US-09-106-194-2           Sequence 2, Appli
        41     10       2.1   1001    2   US-08-884-569A-2          Sequence 2, Appli
        42      9       1.9     26    2   US-09-336-536-59          Sequence 59, Appl
```

This page gives you Search Results detail for the Application 10680755 and Search Result us-10-680-755a-1.olig-n2p.rapbm.

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OM nucleic - protein search, using frame_plus_n2p model

Run on:        June 20, 2006, 08:51:16 ; Search time 52 Seconds
                                         (without alignments)
                                         3997.901 Million cell updates/sec

Title:         US-10-680-755A-1
Perfect score: 480
Sequence:      1 cgcccttactcactataggg..........aaaaaaaatatgcggccgcg 1496

Scoring table: OLIGO
               Xgapop 60.0 , Xgapext 60.0
               Ygapop 60.0 , Ygapext 60.0
               Fgapop 60.0 , Fgapext  7.0
               Delop  60.0 , Delext  60.0

Searched:      2097797 seqs, 463214858 residues

Word size:     1

Total number of hits satisfying chosen parameters:      3993348

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10680755/runat_19062006_173229_21719/app_query.fasta_1
-DB=Published_Applications_AA_Main -QFMT=fastan -SUFFIX=olig-n2p.rapbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=50 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02p
-USER=US10680755_@CGN_1_1_342_@runat_19062006_173229_21719 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60
```

```
Database :       Published_Applications_AA_Main:*
                 1:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                 2:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                 3:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
                 4:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                 5:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                 6:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	108	22.5	108	4	US-10-016-481-5	Sequence 5, Appli
2	108	22.5	108	4	US-10-231-411-4	Sequence 4, Appli
3	108	22.5	108	4	US-10-212-355-2	Sequence 2, Appli
4	108	22.5	108	4	US-10-323-157-5	Sequence 5, Appli
5	108	22.5	108	4	US-10-212-201-2	Sequence 2, Appli
6	108	22.5	108	4	US-10-467-019-17	Sequence 17, Appl
7	108	22.5	108	4	US-10-680-755A-2	Sequence 2, Appli
8	108	22.5	108	4	US-10-680-800A-2	Sequence 2, Appli
9	108	22.5	108	5	US-10-713-567-5	Sequence 5, Appli
10	108	22.5	108	5	US-10-811-328-5	Sequence 5, Appli
11	108	22.5	108	5	US-10-912-907-5	Sequence 5, Appli
12	108	22.5	108	5	US-10-415-724-5	Sequence 5, Appli
13	108	22.5	108	5	US-10-990-246-2	Sequence 2, Appli
14	108	22.5	108	5	US-10-503-554A-17	Sequence 17, Appl
15	108	22.5	108	5	US-10-982-168-2	Sequence 2, Appli
16	108	22.5	108	5	US-10-504-588-6	Sequence 6, Appli
17	108	22.5	116	4	US-10-680-755A-26	Sequence 26, Appl
18	108	22.5	116	4	US-10-680-800A-26	Sequence 26, Appl
19	87	18.1	100	3	US-09-886-242A-4	Sequence 4, Appli
20	87	18.1	100	4	US-10-027-603-4	Sequence 4, Appli
21	87	18.1	100	5	US-10-692-299-4	Sequence 4, Appli
22	81	16.9	81	4	US-10-016-481-6	Sequence 6, Appli
23	81	16.9	81	4	US-10-323-157-6	Sequence 6, Appli
24	81	16.9	81	4	US-10-417-426-5	Sequence 5, Appli
25	81	16.9	81	4	US-10-467-019-19	Sequence 19, Appl
26	81	16.9	81	5	US-10-680-554-7	Sequence 7, Appli
27	81	16.9	81	5	US-10-713-567-6	Sequence 6, Appli
28	81	16.9	81	5	US-10-811-328-6	Sequence 6, Appli
29	81	16.9	81	5	US-10-912-907-6	Sequence 6, Appli
30	81	16.9	81	5	US-10-415-724-6	Sequence 6, Appli
31	81	16.9	81	5	US-10-977-113-9	Sequence 9, Appli
32	81	16.9	81	5	US-10-871-152-18	Sequence 18, Appl
33	81	16.9	81	5	US-10-503-554A-19	Sequence 19, Appl
34	81	16.9	81	6	US-11-073-420-9	Sequence 9, Appli
35	80	16.7	80	4	US-10-467-019-22	Sequence 22, Appl
36	80	16.7	80	5	US-10-503-554A-22	Sequence 22, Appl
37	74	15.4	129	4	US-10-132-812-14	Sequence 14, Appl
38	74	15.4	129	4	US-10-231-411-2	Sequence 2, Appli
39	74	15.4	129	4	US-10-680-755A-29	Sequence 29, Appl
40	74	15.4	129	4	US-10-680-800A-29	Sequence 29, Appl
41	53	11.0	108	5	US-10-713-567-34	Sequence 34, Appl
42	53	11.0	108	5	US-10-977-113-6	Sequence 6, Appli
43	53	11.0	108	6	US-11-073-420-6	Sequence 6, Appli

SCORE Search Results Details for Application 10680755 and Search Result us-10-680-755a-1.olig-n2p.rapbn.

Score Home Page   Retrieve Application List   SCORE System Overview   SCORE FAQ   Comments / Suggestions

This page gives you Search Results detail for the Application 10680755 and Search Result us-10-680-755a-1.olig-n2p.rapbn.

start

Go Back to previous page

```
                    GenCore version 5.1.9
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OM nucleic - protein search, using frame_plus_n2p model

Run on:          June 20, 2006, 08:52:21 ; Search time 3.9 Seconds
                                          (without alignments)
                                          2595.748 Million cell updates/sec

Title:           US-10-680-755A-1
Perfect score:   480
Sequence:        1 cgcccttactcactataggg..........aaaaaaaatatgcggccgcg 1496

Scoring table:   OLIGO
                 Xgapop 60.0 , Xgapext 60.0
                 Ygapop 60.0 , Ygapext 60.0
                 Fgapop 60.0 , Fgapext  7.0
                 Delop  60.0 , Delext  60.0

Searched:        96747 seqs, 22556637 residues

Word size:       1

Total number of hits satisfying chosen parameters:      187790

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10680755/runat_19062006_173232_21785/app_query.fasta_1
-DB=Published_Applications_AA_New -QFMT=fastan -SUFFIX=olig-n2p.rapbn
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=100 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1
-ALIGN=50 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abss02p
-USER=US10680755_@CGN_1_1_16_@runat_19062006_173232_21785 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60
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Database :        Published_Applications_AA_New:*
                  1:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                  2:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                  3:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                  4:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                  5:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                  6:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                  7:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                  8:  /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	13	2.7	423	6	US-10-449-902-47387	Sequence 47387, A
2	11	2.3	26	7	US-11-154-977-79	Sequence 79, Appl
3	11	2.3	53	7	US-11-154-977-73	Sequence 73, Appl
4	11	2.3	117	7	US-11-154-977-71	Sequence 71, Appl
5	11	2.3	121	7	US-11-154-977-75	Sequence 75, Appl
6	11	2.3	144	7	US-11-154-977-59	Sequence 59, Appl
7	11	2.3	144	7	US-11-154-977-77	Sequence 77, Appl
8	11	2.3	148	7	US-11-154-977-65	Sequence 65, Appl
9	11	2.3	171	7	US-11-154-977-67	Sequence 67, Appl
10	11	2.3	173	7	US-11-154-977-47	Sequence 47, Appl
11	11	2.3	200	7	US-11-154-977-41	Sequence 41, Appl
12	11	2.3	212	7	US-11-154-977-61	Sequence 61, Appl
13	11	2.3	235	7	US-11-154-977-63	Sequence 63, Appl
14	11	2.3	239	7	US-11-154-977-51	Sequence 51, Appl
15	11	2.3	239	7	US-11-154-977-69	Sequence 69, Appl
16	11	2.3	262	7	US-11-154-977-53	Sequence 53, Appl
17	11	2.3	264	7	US-11-154-977-39	Sequence 39, Appl
18	11	2.3	266	7	US-11-154-977-57	Sequence 57, Appl
19	11	2.3	268	7	US-11-154-977-43	Sequence 43, Appl
20	11	2.3	291	7	US-11-154-977-27	Sequence 27, Appl
21	11	2.3	291	7	US-11-154-977-45	Sequence 45, Appl
22	11	2.3	295	7	US-11-154-977-33	Sequence 33, Appl
23	11	2.3	318	7	US-11-154-977-35	Sequence 35, Appl
24	11	2.3	324	7	US-11-154-977-8	Sequence 8, Appli
25	11	2.3	330	7	US-11-154-977-55	Sequence 55, Appl
26	11	2.3	357	7	US-11-154-977-49	Sequence 49, Appl
27	11	2.3	359	7	US-11-154-977-29	Sequence 29, Appl
28	11	2.3	382	7	US-11-154-977-31	Sequence 31, Appl
29	11	2.3	386	7	US-11-154-977-19	Sequence 19, Appl
30	11	2.3	386	7	US-11-154-977-37	Sequence 37, Appl
31	11	2.3	409	7	US-11-154-977-21	Sequence 21, Appl
32	11	2.3	413	7	US-11-154-977-25	Sequence 25, Appl
33	11	2.3	477	7	US-11-154-977-23	Sequence 23, Appl
34	11	2.3	504	7	US-11-154-977-17	Sequence 17, Appl
35	11	2.3	504	7	US-11-154-977-153	Sequence 153, App
36	10	2.1	183	7	US-11-284-236-112	Sequence 112, App
37	10	2.1	231	6	US-10-953-349-35556	Sequence 35556, A
38	10	2.1	251	6	US-10-953-349-35555	Sequence 35555, A
39	10	2.1	309	6	US-10-449-902-51144	Sequence 51144, A
40	10	2.1	464	6	US-10-505-928-757	Sequence 757, App
41	9	1.9	92	6	US-10-953-349-25928	Sequence 25928, A

This page gives you Search Results detail for the Application 10680755 and Search start

```
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OM nucleic - protein search, using frame_plus_n2p model

Run on:          June 20, 2006, 08:05:51 ; Search time 11.9 Seconds
                                           (without alignments)
                                           3628.746 Million cell updates/sec

Title:           US-10-680-755A-1
Perfect score:   480
Sequence:        1 cgcccttactcactataggg..........aaaaaaaatatgcggccgcg 1496

Scoring table:   OLIGO
                 Xgapop 60.0 , Xgapext 60.0
                 Ygapop 60.0 , Ygapext 60.0
                 Fgapop 60.0 , Fgapext  7.0
                 Delop  60.0 , Delext  60.0

Searched:        283416 seqs, 96216763 residues

Word size:       1

Total number of hits satisfying chosen parameters:      565918

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10680755/runat_19062006_173217_21491/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=olig-n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=50 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10680755_@CGN_1_1_63_@runat_19062006_173217_21491 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database :       PIR_80:*
                 1:  pir1:*
                 2:  pir2:*
                 3:  pir3:*
                 4:  pir4:*

     Pred. No. is the number of results predicted by chance to have a
```

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	12	2.5	131	1	SEPG	secretin precursor
	2	12	2.5	1061	1	OYHUAR	natriuretic peptid
c	3	10	2.1	405	4	A61181	homeotic protein H
	4	10	2.1	418	2	T52071	mRNA-binding prote
	5	10	2.1	602	2	A35564	prostaglandin-endo
	6	9	1.9	101	2	B28414	growth-regulated p
c	7	9	1.9	136	2	F75309	hypothetical prote
c	8	9	1.9	201	1	S16262	auxin-binding prot
	9	9	1.9	235	2	I38440	flt3 ligand - huma
	10	9	1.9	238	2	I38849	LERK-3 - human
	11	9	1.9	310	2	A60967	insulin-like growt
	12	9	1.9	317	2	I46916	insulin-like growt
	13	9	1.9	491	2	JC6197	stromelysin 3 (EC
	14	9	1.9	536	1	C64728	probable membrane
	15	9	1.9	536	2	G85488	probable transport
	16	9	1.9	536	2	G90637	probable transport
	17	9	1.9	552	1	WJFFEN	homeotic protein e
	18	9	1.9	602	2	S39782	cyclooxygenase 1 -
	19	9	1.9	602	2	S69198	prostaglandin G/H
	20	9	1.9	682	2	T47473	receptor-like prot
	21	9	1.9	1015	2	JC5062	phogrin precursor
	22	9	1.9	1015	2	JC5263	transmembrane tyro
	23	9	1.9	1019	2	T00117	dve protein - frui
	24	9	1.9	1057	1	OYMSAR	atrial natriuretic
	25	9	1.9	1057	1	OYRTR	atrial natriuretic
	26	9	1.9	1057	2	I55319	guanylyl cyclase A
	27	9	1.9	1057	2	I57963	natriuretic peptid
	28	9	1.9	1062	2	T46444	hypothetical prote
	29	9	1.9	1102	2	JC6316	probable protein k
	30	9	1.9	1110	1	S55279	guanylate cyclase
	31	9	1.9	1113	2	T00271	hypothetical prote
	32	9	1.9	1313	1	JC2038	peptidyl-dipeptida
c	33	9	1.9	1533	2	A46221	abdominal segment
	34	9	1.9	1584	2	T00026	brain-specific ang
	35	9	1.9	2496	2	A71616	secreted protein P
	36	9	1.9	2499	1	A30788	mannose 6-phosphat
	37	8	1.7	51	2	T07340	hypothetical prote
c	38	8	1.7	54	2	T07354	NADH dehydrogenase
	39	8	1.7	61	1	DNVPBF	DNA-binding protei
c	40	8	1.7	71	2	AG2846	cold shock protein
c	41	8	1.7	71	2	H97623	hypothetical prote
	42	8	1.7	77	2	A03982	p15E protein - sim
c	43	8	1.7	83	2	AD3314	cold shock protein
	44	8	1.7	94	2	T03285	anther-specific pr
	45	8	1.7	106	2	T06479	proline/leucine-ri
	46	8	1.7	107	2	C86477	protein F15O4.29 [
	47	8	1.7	120	2	AC3550	NAD(P) transhydrog
	48	8	1.7	125	2	C83138	hypothetical prote
	49	8	1.7	132	2	S43488	homeotic protein L
	50	8	1.7	134	2	A40959	secretin precursor
	51	8	1.7	142	2	S54481	hypothetical prote
	52	8	1.7	150	2	S42203	avidin-related pro
	53	8	1.7	150	2	S42201	avidin-related pro

This page gives you Search Results detail for the Application 10680755 and Search start

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OM nucleic - protein search, using frame_plus_n2p model

Run on: June 20, 2006, 08:05:51 ; Search time 11.9 Seconds
                                           (without alignments)
                                           3628.746 Million cell updates/sec

Title: US-10-680-755A-1
Perfect score: 480
Sequence: 1 cgcccttactcactataggg..........aaaaaaaatatgcggccgcg 1496

Scoring table: OLIGO
                 Xgapop 60.0 , Xgapext 60.0
                 Ygapop 60.0 , Ygapext 60.0
                 Fgapop 60.0 , Fgapext 7.0
                 Delop 60.0 , Delext 60.0

Searched: 283416 seqs, 96216763 residues

Word size: 1

Total number of hits satisfying chosen parameters: 565918

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10680755/runat_19062006_173217_21491/app_query.fasta_1
-DB=PIR -QFMT=fastan -SUFFIX=olig-n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi -LIST=100
-DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=50 -MODE=LOCAL -OUTFMT=pto
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10680755_@CGN_1_1_63_@runat_19062006_173217_21491 -NCPU=6 -ICPU=3
-NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=60 -DELEXT=60

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	12	2.5	131	1	SEPG	secretin precursor
2	12	2.5	1061	1	OYHUAR	natriuretic peptid
c 3	10	2.1	405	4	A61181	homeotic protein H
4	10	2.1	418	2	T52071	mRNA-binding prote
5	10	2.1	602	2	A35564	prostaglandin-endo
6	9	1.9	101	2	B28414	growth-regulated p
c 7	9	1.9	136	2	F75309	hypothetical prote
c 8	9	1.9	201	1	S16262	auxin-binding prot
9	9	1.9	235	2	I38440	flt3 ligand - huma
10	9	1.9	238	2	I38849	LERK-3 - human
11	9	1.9	310	2	A60967	insulin-like growt
12	9	1.9	317	2	I46916	insulin-like growt
13	9	1.9	491	2	JC6197	stromelysin 3 (EC
14	9	1.9	536	1	C64728	probable membrane
15	9	1.9	536	2	G85488	probable transport
16	9	1.9	536	2	G90637	probable transport
17	9	1.9	552	1	WJFFEN	homeotic protein e
18	9	1.9	602	2	S39782	cyclooxygenase 1 -
19	9	1.9	602	2	S69198	prostaglandin G/H
20	9	1.9	682	2	T47473	receptor-like prot
21	9	1.9	1015	2	JC5062	phogrin precursor
22	9	1.9	1015	2	JC5263	transmembrane tyro
23	9	1.9	1019	2	T00117	dve protein - frui
24	9	1.9	1057	1	OYMSAR	atrial natriuretic
25	9	1.9	1057	1	OYRTR	atrial natriuretic
26	9	1.9	1057	2	I55319	guanylyl cyclase A
27	9	1.9	1057	2	I57963	natriuretic peptid
28	9	1.9	1062	2	T46444	hypothetical prote
29	9	1.9	1102	2	JC6316	probable protein k
30	9	1.9	1110	1	S55279	guanylate cyclase
31	9	1.9	1113	2	T00271	hypothetical prote
32	9	1.9	1313	1	JC2038	peptidyl-dipeptida
c 33	9	1.9	1533	2	A46221	abdominal segment
34	9	1.9	1584	2	T00026	brain-specific ang
35	9	1.9	2496	2	A71616	secreted protein P
36	9	1.9	2499	1	A30788	mannose 6-phosphat
37	8	1.7	51	2	T07340	hypothetical prote
c 38	8	1.7	54	2	T07354	NADH dehydrogenase
39	8	1.7	61	1	DNVPBF	DNA-binding protei
c 40	8	1.7	71	2	AG2846	cold shock protein
c 41	8	1.7	71	2	H97623	hypothetical prote
42	8	1.7	77	2	A03982	p15E protein - sim
c 43	8	1.7	83	2	AD3314	cold shock protein
44	8	1.7	94	2	T03285	anther-specific pr
45	8	1.7	106	2	T06479	proline/leucine-ri
46	8	1.7	107	2	C86477	protein F15O4.29 [
47	8	1.7	120	2	AC3550	NAD(P) transhydrog
48	8	1.7	125	2	C83138	hypothetical prote
49	8	1.7	132	2	S43488	homeotic protein L
50	8	1.7	134	2	A40959	secretin precursor
51	8	1.7	142	2	S54481	hypothetical prote
52	8	1.7	150	2	S42203	avidin-related pro
53	8	1.7	150	2	S42201	avidin-related pro

SCORE Search Results Details for Applicati(10680755 and Search Result us-10-680-75! 1.olig.rni.

This page gives you Search Results detail for the Application 10680755 and Search us-10-680-755a-1.olig.rni.

start

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OM nucleic - nucleic search, using sw model

Run on:            June 19, 2006, 23:42:14 ; Search time 312 Seconds
                                            (without alignments)
                                            8971.727 Million cell updates/sec

Title:             US-10-680-755A-1
Perfect score:     1496
Sequence:          1 cgcccttactcactataggg..........aaaaaaaatatgcggccgcg 1496

Scoring table:     OLIGO_NUC
                   Gapop 60.0 , Gapext 60.0

Searched:          1403666 seqs, 935554401 residues

Word size :        1

Total number of hits satisfying chosen parameters:      2806514

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :         Issued_Patents_NA:*
                   1:  /EMC_Celerra_SIDS3/ptodata/2/ina/1_COMB.seq:*
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                   3:  /EMC_Celerra_SIDS3/ptodata/2/ina/6A_COMB.seq:*
                   4:  /EMC_Celerra_SIDS3/ptodata/2/ina/6B_COMB.seq:*
                   5:  /EMC_Celerra_SIDS3/ptodata/2/ina/7_COMB.seq:*
                   6:  /EMC_Celerra_SIDS3/ptodata/2/ina/H_COMB.seq:*
                   7:  /EMC_Celerra_SIDS3/ptodata/2/ina/PCTUS_COMB.seq:*
                   8:  /EMC_Celerra_SIDS3/ptodata/2/ina/PP_COMB.seq:*
                   9:  /EMC_Celerra_SIDS3/ptodata/2/ina/RE_COMB.seq:*
                   10:  /EMC_Celerra_SIDS3/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.
```

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1496	100.0	1496	3	US-09-712-529-1	Sequence 1, Appli
	2	1496	100.0	1496	3	US-10-212-201A-1	Sequence 1, Appli
	3	1496	100.0	1496	3	US-10-212-355-1	Sequence 1, Appli
	4	705	47.1	1116	3	US-09-023-655-617	Sequence 617, App
	5	50	3.3	50	3	US-10-131-827-832	Sequence 832, App
	6	50	3.3	50	5	US-10-131-831-832	Sequence 832, App
	7	44	2.9	4439	3	US-09-668-313A-17	Sequence 17, Appl
c	8	43	2.9	660	3	US-09-417-822-41	Sequence 41, Appl
c	9	43	2.9	660	3	US-09-957-837A-41	Sequence 41, Appl
	10	43	2.9	944	3	US-09-070-526-1	Sequence 1, Appli
	11	41	2.7	1342	3	US-08-832-399-1	Sequence 1, Appli
	12	41	2.7	1342	3	US-09-372-498-1	Sequence 1, Appli
	13	40	2.7	2345	3	US-10-136-227A-29	Sequence 29, Appl
	14	40	2.7	2345	3	US-09-981-649A-29	Sequence 29, Appl
	15	40	2.7	2360	3	US-10-136-227A-27	Sequence 27, Appl
	16	40	2.7	2360	3	US-09-981-649A-27	Sequence 27, Appl
c	17	39	2.6	443	3	US-09-417-822-43	Sequence 43, Appl
c	18	39	2.6	443	3	US-09-957-837A-43	Sequence 43, Appl
c	19	39	2.6	909	3	US-09-035-648-19	Sequence 19, Appl
c	20	39	2.6	909	3	US-09-001-951-19	Sequence 19, Appl
c	21	39	2.6	909	3	US-08-818-829-19	Sequence 19, Appl
	22	39	2.6	1273	3	US-09-910-695-9	Sequence 9, Appli
	23	39	2.6	1383	3	US-09-328-475C-338	Sequence 338, App
	24	39	2.6	1813	3	US-09-620-312D-29	Sequence 29, Appl
	25	38	2.5	1888	3	US-09-035-648-20	Sequence 20, Appl
	26	38	2.5	1888	3	US-09-001-951-20	Sequence 20, Appl
	27	38	2.5	1888	3	US-08-818-829-20	Sequence 20, Appl
	28	38	2.5	4203	2	US-08-866-757-1	Sequence 1, Appli
	29	38	2.5	4203	3	US-09-153-593-1	Sequence 1, Appli
	30	37	2.5	45	3	US-09-284-782-5	Sequence 5, Appli
	31	37	2.5	461	2	US-08-621-502A-8	Sequence 8, Appli
	32	37	2.5	1024	3	US-09-328-475C-37	Sequence 37, Appl
c	33	37	2.5	1178	4	US-10-080-960-10	Sequence 10, Appl
	34	37	2.5	1352	4	US-10-080-960-7	Sequence 7, Appli
c	35	37	2.5	1502	2	US-08-651-940-1	Sequence 1, Appli
c	36	37	2.5	1502	3	US-09-295-029-1	Sequence 1, Appli
c	37	37	2.5	1502	3	US-09-724-768-1	Sequence 1, Appli
	38	37	2.5	2198	4	US-10-044-205A-1	Sequence 1, Appli
	39	37	2.5	2859	3	US-09-923-684-2	Sequence 2, Appli
	40	37	2.5	3920	3	US-09-923-684-1	Sequence 1, Appli
	41	36	2.4	44	2	US-08-381-572-5	Sequence 5, Appli
	42	36	2.4	44	2	US-08-381-572-6	Sequence 6, Appli
	43	36	2.4	44	2	US-08-592-820-5	Sequence 5, Appli
	44	36	2.4	44	2	US-08-592-820-6	Sequence 6, Appli
	45	36	2.4	44	2	US-08-670-707A-13	Sequence 13, Appl
	46	36	2.4	44	3	US-09-037-601-13	Sequence 13, Appl
	47	36	2.4	44	3	US-09-234-393-5	Sequence 5, Appli
	48	36	2.4	44	3	US-09-124-238A-19	Sequence 19, Appl
	49	36	2.4	44	3	US-09-323-873A-23	Sequence 23, Appl
	50	36	2.4	44	3	US-09-570-367C-4	Sequence 4, Appli
	51	36	2.4	44	3	US-09-165-239A-6	Sequence 6, Appli
	52	36	2.4	44	3	US-09-315-179-13	Sequence 13, Appl
	53	36	2.4	44	3	US-09-182-145-41	Sequence 41, Appl
	54	36	2.4	44	3	US-09-721-975-19	Sequence 19, Appl
	55	36	2.4	44	3	US-09-865-171-5	Sequence 5, Appli